

SEQUENCE LISTING

<110> Fletcher, Jonathan A.  
Kroll, Todd G.

<120> PAX8-PPARGgamma NUCLEIC ACID MOLECULES  
AND POLYPEPTIDES AND USES THEREOF

<130> B0801/7196 (ERP/MAT)

<150> US 60/177,109

<151> 2000-01-20

<150> US 60/225,079

<151> 2000-08-14

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<170> FastSEQ for Windows Version 3.0

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<211> 2334

<212> DNA

<213> Homo Sapiens

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<221> CDS

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gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag	96
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
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cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct	144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg	192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
50 55 60	
tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
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ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	

0976544.011001

cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctc ctg	336
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
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 gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att	384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
 aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg	432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
130 135 140	
 gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc	480
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
145 150 155 160	
 ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg	528
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	
 ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc	576
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	
 agc gac aag agg aaa atg gat gac agt gat cag gat agc tgc cga cta	624
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu	
195 200 205	
 agc att gac tca cag agc agc agc agc gga ccc cga aag cac ctt cgc	672
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg	
210 215 220	
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Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe	
225 230 235 240	
 gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc cac acc aaa	768
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys	
245 250 255	
 ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc acc ctg gac	816
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
260 265 270	
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Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn	
275 280 285	
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Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Glu Met Thr Met Val	
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 gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg	960
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	
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Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	
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att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac	1104
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	
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Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	
370 375 380	
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Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu	
385 390 395 400	
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Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp	
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aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag	1296
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys	
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Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys	
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gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac	1392
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr	
450 455 460	
tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc	1440
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile	
465 470 475 480	
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Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu	
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Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg	
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gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg	1584
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Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu	
565 570 575	
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Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn	
595 600 605	
ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag	1872
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Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu	
645 650 655	
cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg	2016
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val	
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Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile	
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Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys	
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ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc	2208
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu	
725 730 735	
cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta	2256
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu	
740 745 750	
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2334

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Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	Glu	Asp
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Pro Pro Tyr Tyr Ser Glu	Lys Thr Gln Leu Tyr	Asn Lys Pro His Glu
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Glu Pro Ser Asn Ser Leu	Met Ala Ile Glu Cys	Arg Val Cys Gly Asp
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Lys Ala Ser Gly Phe His	Tyr Gly Val His Ala	Cys Glu Gly Cys Lys
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Cys Arg Phe Gln Lys Cys	Leu Ala Val Gly Met	Ser His Asn Ala Ile
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Ile Ser Ser Asp Ile Asp	Gln Leu Asn Pro Glu	Ser Ala Asp Leu Arg
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Lys Ile Lys Phe Lys His	Ile Thr Pro Leu Gln	Glu Gln Ser Lys Glu
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Arg Lys Pro Phe Gly Asp	Phe Met Glu Pro Lys	Phe Glu Phe Ala Val
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Lys Phe Asn Ala Leu Glu	Leu Asp Asp Ser Asp	Leu Ala Ile Phe Ile
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Ala Val Ile Ile Leu Ser	Gly Asp Arg Pro Gly	Leu Leu Asn Val Lys
690	695	700
Pro Ile Glu Asp Ile Gln	Asp Asn Leu Leu Gln	Ala Leu Glu Leu Gln
705	710	715
Leu Lys Leu Asn His Pro	Glu Ser Ser Gln Leu	Phe Ala Lys Leu Leu
725	730	735
Gln Lys Met Thr Asp Leu	Arg Gln Ile Val Thr	Glu His Val Gln Leu
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gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag	96
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
20 25 30	
cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct	144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
cgc cag ctg cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg	192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
50 55 60	
tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
65 70 75 80	
ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	
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Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
100 105 110	
gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att	384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctg cct atg	432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
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Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
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Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	
ggc tcc acc tac tcc atc aat ggg ctg ctg ggc atc gct cag cct ggc	576
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
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Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro	
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Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly	
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ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat	1536
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Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala	
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Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro	
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Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
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Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
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Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
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Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
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Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
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Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
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Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg	
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Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys	
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Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
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Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro	
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Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe	
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Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu	
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2625

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Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln
		20						25					30		
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
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Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
	50					55					60				
Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys
65					70					75					80
Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
				85					90					95	
Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
			100					105					110		
Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
		115						120				125			
Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
	130					135					140				
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
145					150					155					160
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
			165						170					175	
Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Gly	Ile	Ala	Gln	Pro	Gly	
		180						185				190			
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
	195						200					205			
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg
	210					215					220				
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225					230					235					240
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
			245						250					255	
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
		260						265					270		
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
	275						280					285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro
	290					295					300				
Leu	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser	Thr
305					310					315					320
Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
			325						330					335	
Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
			340					345					350		
Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val	Gly

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355	360	365
Pro Thr Leu Pro Gly Tyr	Pro Pro His Ile	Pro Thr Ser Gly Gln Gly
370	375	380
Ser Tyr Ala Ser Ser Ala	Ile Ala Gly Met Val	Ala Glu Met Thr Met
385	390	395
Val Asp Thr Glu Met Pro Phe Trp	Pro Thr Asn Phe Gly Ile Ser Ser	
405	410	415
Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys		
420	425	430
Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu		
435	440	445
Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr		
450	455	460
Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala		
465	470	475
Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His		
485	490	495
Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly		
500	505	510
Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys		
515	520	525
Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg		
530	535	540
Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln		
545	550	555
Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala		
565	570	575
Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala		
580	585	590
Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu		
595	600	605
Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro		
610	615	620
Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp		
625	630	635
Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu		
645	650	655
Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys		
660	665	670
Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu		
675	680	685
Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val		
690	695	700
Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His		
705	710	715
Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val		
725	730	735
Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser		
740	745	750
Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala		
755	760	765
Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe		
770	775	780
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val		
785	790	795
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu		

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	805		810		815
Gln Leu Lys	Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu				
	820		825		830
Leu Gln Lys	Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln				
	835		840		845
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro					
	850		855		860
Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr					
865	870				

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 Thr Tyr Pro Val Val Ala Glu Met Thr Met Val Asp Thr  
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 Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr  
 1 5 10

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<400> 10  
 Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr

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5

10

<210> 11  
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<212> DNA  
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<220>  
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<222> (3)...(41)

<400> 11

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Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr  
1 5 10

<210> 12  
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<400> 12

Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr  
1 5 10

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<212> DNA  
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<220>  
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<222> (11)...(1363)

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Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu  
1 5 10

aac cag ctg gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg 97  
Asn Gln Leu Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val  
15 20 25

gtc cgc cag cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc 145  
Val Arg Gln Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys  
30 35 40 45

gac atc tct cgc cag ctc cgc gtc agc cat ggt tgc gtc agc aag atc 193  
Asp Ile Ser Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile  
50 55 60

ctt ggc agg tac tac gag act ggc agc atc cgg cct gga gtg ata ggg 241  
Leu Gly Arg Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly  
65 70 75

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ggc tcc aag ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg	289
Gly Ser Lys Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly	
80 85 90	
gac tac aaa cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac	337
Asp Tyr Lys Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp	
95 100 105	
cgg ctg ctg gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc	385
Arg Leu Leu Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val	
110 115 120 125	
agc tcc att aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac	433
Ser Ser Ile Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn	
130 135 140	
ctc cct atg gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac	481
Leu Pro Met Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His	
145 150 155	
acg ctg atc ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg	529
Thr Leu Ile Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser	
160 165 170	
gat tcc ctg ggc tcc acc tac tcc atc aat ggg ctg ctg ggc atc gct	577
Asp Ser Leu Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala	
175 180 185	
cag cct ggc agc gac aag agg aaa atg gat gac agt gat cag gat agc	625
Gln Pro Gly Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser	
190 195 200 205	
tgc cga cta agc att gac tca cag agc agc agc agc gga ccc cga aag	673
Cys Arg Leu Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys	
210 215 220	
cac ctt cgc acg gat gcc ttc agc cag cac cac ctg gag ccg ctg gag	721
His Leu Arg Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu	
225 230 235	
tgc cca ttt gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc	769
Cys Pro Phe Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser	
240 245 250	
cac acc aaa ggc gag cag ggc ctg tac ccg ctg ccc ttg ctg aac agc	817
His Thr Lys Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser	
255 260 265	
acc ctg gac gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg	865
Thr Leu Asp Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu	
270 275 280 285	
ggg cgc aac ctg tcg act cac cag acc tac ccc gtg gtg gca gat cct	913
Gly Arg Asn Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro	
290 295 300	

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cac tca ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct 961  
His Ser Pro Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser  
305 310 315

agc tcc acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag 1009  
Ser Ser Thr Pro Ser Ser Leu Ser Ser Ser Ala Phe Leu Asp Leu Gln  
320 325 330

caa gtc ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc 1057  
Gln Val Gly Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala  
335 340 345

tcc gtg tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag 1105  
Ser Val Tyr Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu  
350 355 360 365

atg gtg ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc 1153  
Met Val Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser  
370 375 380

gga cag ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga 1201  
Gly Gln Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly  
385 390 395

agt gaa tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac 1249  
Ser Glu Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr  
400 405 410

agc gag gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat 1297  
Ser Glu Ala Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr  
415 420 425

tat tac agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg 1345  
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430 435 440 445

gcc ttt gac cat ctg tag ttgaagctt 1372  
Ala Phe Asp His Leu \*  
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Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
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			Met Gly	Glu Thr	Leu Gly Asp	
			1		5	
cct att gac	cca gaa agc	gat tcc ttc	act gat aca	ctg tct gca	aac	162
Ser						
ata tca caa	gaa atg acc	atg gtt gac	aca gag atg	cca ttc tgg	ccc	210
Pro Ile Asp	Pro Glu Ser	Asp Ser Phe	Thr Asp Thr	Leu Ser Ala	Asn	
10		15		20		
acc aac ttt	ggg atc agc	tcc gtg gat	ctc tcc gta	atg gaa gac	cac	258
Ile Ser Gln	Glu Met Thr	Met Val Asp	Thr Glu Met	Pro Phe Trp	Pro	
25		30		35	40	
tcc cac tcc	ttt gat atc	aag ccc ttc	act act gtt	gac ttc tcc	agc	306
Thr Asn Phe	Gly Ile Ser	Ser Val Asp	Leu Ser Val	Met Glu Asp	His	
	45		50		55	
att tct act	cca cat tac	gaa gac att	cca ttc aca	aga aca gat	cca	354
Ser His Ser	Phe Asp Ile	Lys Pro Phe	Thr Thr Val	Asp Phe Ser	Ser	
	60		65		70	
gtg gtt gca	gat tac aag	tat gac ctg	aaa ctt caa	gag tac caa	agt	402
Ile Ser Thr	Pro His Tyr	Glu Asp Ile	Pro Phe Thr	Arg Thr Asp	Pro	
	75		80		85	
gca atc aaa	gtg gag cct	gca tct cca	cct tat tat	tct gag aag	act	450
Val Val Ala	Asp Tyr Lys	Tyr Asp Leu	Lys Leu Gln	Glu Tyr Gln	Ser	
	90		95		100	
cag ctc tac	aat aag cct	cat gaa gag	cct tcc aac	tcc ctc atg	gca	498
Ala Ile Lys	Val Glu Pro	Ala Ser Pro	Pro Tyr Tyr	Ser Glu Lys	Thr	
105		110		115	120	
att gaa tgt	cgt gtc tgt	gga gat aaa	gct tct gga	ttt cac tat	gga	546
Gln Leu Tyr	Asn Lys Pro	His Glu Glu	Pro Ser Asn	Ser Leu Met	Ala	
	125		130		135	
gtt cat gct	tgt gaa gga	tgc aag ggt	ttc ttc cgg	aga aca atc	aga	594
Ile Glu Cys	Arg Val Cys	Gly Asp Lys	Ala Ser Gly	Phe His Tyr	Gly	
	140		145		150	
ttg aag ctt	atc tat gac	aga tgt gat	ctt aac tgt	cgg atc cac	aaa	642
Val His Ala	Cys Glu Gly	Cys Lys Gly	Phe Phe Arg	Arg Thr Ile	Arg	
	155		160		165	
aaa agt aga	aat aaa tgt	cag tac tgt	cgg ttt cag	aaa tgc ctt	gca	690
Leu Lys Leu	Ile Tyr Asp	Arg Cys Asp	Leu Asn Cys	Arg Ile His	Lys	
	170		175		180	

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Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala	
185 190 195 200	
gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag ctg	786
Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln Ala	
205 210 215	
aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat gac	834
Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu	
220 225 230	
tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg atc	882
Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp	
235 240 245	
ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac atg	930
Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile	
250 255 260	
aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc acc	978
Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met	
265 270 275 280	
ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag ggc	1026
Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr	
285 290 295	
tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat gcc	1074
Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly	
300 305 310	
aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta act	1122
Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala	
315 320 325	
ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc tcc	1170
Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr	
330 335 340	
ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc atg	1218
Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser	
345 350 355 360	
aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt atg	1266
Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met	
365 370 375	
gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta gat	1314
Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met	
380 385 390	
gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga gac	1362
Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp	
395 400 405	

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cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac aac 1410  
 Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp  
 410 415 420

ctg cta caa gcc ctg gag ctc cag ctg aag ctg aac cac cct gag tcc 1458  
 Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn  
 425 430 435 440

tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga cag 1506  
 Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser  
 445 450 455

att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg gag 1554  
 Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln  
 460 465 470

aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac ttg 1602  
 Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu  
 475 480 485

tac tag 1608  
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 35 40 45  
 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
 50 55 60  
 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
 65 70 75 80  
 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
 85 90 95  
 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
 100 105 110  
 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
 115 120 125  
 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
 130 135 140  
 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
 145 150 155 160  
 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
 165 170 175  
 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
 180 185 190

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Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	Ile
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		210				215					220				
Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu	Arg
225					230					235					240
Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro	Leu
				245					250					255	
Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp	Lys
			260					265						270	
Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu	Asp
		275					280					285			
Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	Glu
		290				295					300				
Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	Ala
305					310					315					320
Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val	Asn
					325				330					335	
Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Lys	Tyr	Gly	Val	His	Glu	
			340					345					350		
Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val	Leu
		355					360						365		
Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu
		370				375					380				
Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val
385					390					395					400
Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	Phe	Ile
				405					410					415	
Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val	Lys
			420					425						430	
Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu	Leu	Gln
		435					440						445		
Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys	Leu	Leu
		450				455					460				
Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	Gln	Leu
465					470					475					480
Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	Ser	Leu	His	Pro	Leu
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18

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 agccccgagc cctcgggcgg ctgcgagcga ctccccggcg atg cct cac aac tcc 175  
 Met Pro His Asn  
 1

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223  
 Ser  
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aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg 271  
 Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val  
 10 15 20

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc 319  
 Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu  
 25 30 35

agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc 367  
 Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val  
 40 45 50

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Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly	
55 60 65	
ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc	463
Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr	
70 75 80 85	
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Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys Arg Gln Asn Pro Thr	
90 95 100	
gac aat gac act gtg ccc agt gtc agc tcc att aat aga atc atc cgg	559
Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Glu Gly Val Cys	
105 110 115	
acc aaa gtg cag caa cca ttc aac ctc cct atg gac agc tgc gtg gcc	607
Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile Asn Arg Ile Ile Arg	
120 125 130	
acc aag tcc ctg agt ccc gga cac acg ctg atc ccc agc tca gct gta	655
Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met Asp Ser Cys Val Ala	
135 140 145	
act ccc ccg gag tca ccc cag tcg gat tcc ctg ggc tcc acc tac tcc	703
Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile Pro Ser Ser Ala Val	
150 155 160 165	
atc aat ggg ctc ctg ggc atc gct cag cct ggc agc gac aag agg aaa	751
Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu Gly Ser Thr Tyr Ser	
170 175 180	
atg gat gac agt gat cag gat agc tgc cga cta agc att gac tca cag	799
Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly Ser Asp Lys Arg Lys	
185 190 195	
agc agc agc agc gga ccc cga aag cac ctt cgc acg gat gcc ttc agc	847
Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu Ser Ile Asp Ser Gln	
200 205 210	
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Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg Thr Asp Ala Phe Ser	
215 220 225	
cca gag gcc tat gcc tcc ccc agc cac acc aaa ggc gag cag ggc ctc	943
Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr	
230 235 240 245	
tac ccg ctg ccc ttg ctc aac agc acc ctg gac gac ggg aag gcc acc	991
Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu	
250 255 260	
ctg acc cct tcc aac acg cca ctg ggg cgc aac ctc tcg act cac cag	1039
Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr	
265 270 275	

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acc tac ccc gtg gtg gca ggg cga gag atg gtg ggg ccc acg ctg ccc	1087
Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln	
280 285 290	
gga tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc	1135
Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val Gly Pro Thr Leu Pro	
295 300 305	
tct gcc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca gag	1183
Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser	
310 315 320 325	
atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc	1231
Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr Glu	
330 335 340	
gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc ttc act act	1279
Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser	
345 350 355	
gtt gac ttc tcc agc att tct act cca cat tac gaa gac att cca ttc	1327
Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr	
360 365 370	
aca aga aca gat cca gtg gtt gca gat tac aag tat gac ctg aaa ctt	1375
Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe	
375 380 385	
caa gag tac caa agt gca atc aaa gtg gag cct gca tct cca cct tat	1423
Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu	
390 395 400 405	
tat tct gag aag act cag ctc tac aat aag cct cat gaa gag cct tcc	1471
Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr	
410 415 420	
aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa gct tct	1519
Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser	
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Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser	
440 445 450	
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Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe	
455 460 465	
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Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn	
470 475 480 485	
cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc agg ttt ggg	1711
Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe	
490 495 500	

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aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg acc aaa gca Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala 535 540 545	1855
aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa tca cca ttc Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala 550 555 560 565	1903
gtt atc tat gac atg aat tcc tta atg atg gga gaa gat aaa atc aag Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe 570 575 580	1951
ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag gtg gcc atc Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys 585 590 595	1999
cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile 600 605 610	2047
atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt gac ttg Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu 615 620 625	2095
aac gac caa gta act ctc ctc aaa tat gga gtc cac gag atc att tac Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu 630 635 640 645	2143
aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr 650 655 660	2191
ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg cga aag cct Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu 665 670 675	2239
ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg aag ttc aat Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro 680 685 690	2287
gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct gtc att Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn 695 700 705	2335
att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile 710 715 720 725	2383

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Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu  
730 735 740

aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc cag aaa atg 2479  
Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu  
745 750 755

aca gac ctc aga cag att gtc acg gaa cac gtg cag cta ctg cag gtg 2527  
Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met  
760 765 770

atc aag aag acg gag aca gac atg agt ctt cac ccg ctc ctg cag gag 2575  
Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val  
775 780 785

atc tac aag gac ttg tac tag 2596  
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Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95  
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110  
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125  
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140  
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160  
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175  
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190  
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205  
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220

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Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	225	230	235	240
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	245	250	255	
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	260	265	270	
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn	275	280	285	
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Gly	Arg	Glu	Met	Val	290	295	300	
Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln	305	310	315	320
Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Glu	Met	Thr	325	330	335	
Met	Val	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	340	345	350	
Ser	Val	Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	355	360	365	
Lys	Pro	Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	370	375	380	
Glu	Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	385	390	395	400
Tyr	Asp	Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro	405	410	415	
Ala	Ser	Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Lys	Pro	420	425	430	
His	Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	435	440	445	
Gly	Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	450	455	460	
Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	465	470	475	480
Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	485	490	495	
Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	500	505	510	
Ala	Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	515	520	525	
Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	530	535	540	
Leu	Arg	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	545	550	555	560
Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	565	570	575	
Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	580	585	590	
Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	595	600	605	
Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	610	615	620	
Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	625	630	635	640
Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	645	650	655	
His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	660	665	670	

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Val	Leu	Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys
	675						680					685			
Ser	Leu	Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe
	690					695					700				
Ala	Val	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile
705					710					715					720
Phe	Ile	Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn
			725						730					735	
Val	Lys	Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	Ala	Leu	Glu
			740					745					750		
Leu	Gln	Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys
	755						760					765			
Leu	Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val
	770					775					780				
Gln	Leu	Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	Ser	Leu	His
785					790					795					800
Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr					
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agccccgagc	cctcggcggg	ctgcgagcga	ctccccggcg	atg cct cac aac tcc		175
				Met Pro His Asn Ser		
				1	5	
atc aga tct	ggc cat gga	ggg ctg aac	cag ctg gga	ggg gcc ttt	gtg	223
Ile Arg Ser	Gly His Gly	Gly Leu Asn	Gln Leu Gly	Gly Ala Phe	Val	
	10		15		20	
aat ggc aga	cct ctg ccg	gaa gtg gtc	cgc cag cgc	atc gta gac	ctg	271
Asn Gly Arg	Pro Leu Pro	Glu Val Val	Arg Gln Arg	Ile Val Asp	Leu	
	25		30		35	
gcc cac cag	ggt gta agg	ccc tgc gac	atc tct cgc	cag ctc cgc	gtc	319
Ala His Gln	Gly Val Arg	Pro Cys Asp	Ile Ser Arg	Gln Leu Arg	Val	
	40		45		50	
agc cat ggc	tgc gtc agc	aag atc ctt	ggc agg tac	tac gag act	ggc	367
Ser His Gly	Cys Val Ser	Lys Ile Leu	Gly Arg Tyr	Tyr Glu Thr	Gly	
	55		60		65	
agc atc cgg	cct gga gtg	ata ggg ggc	tcc aag ccc	aag gtg gcc	acc	415
Ser Ile Arg	Pro Gly Val	Ile Gly Gly	Ser Lys Pro	Lys Val Ala	Thr	
	70		75		80	
ccc aag gtg	gtg gag aag	att ggg gac	tac aaa cgc	cag aac cct	acc	463

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Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys		
			105					110					115				
gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg	559	
Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg		
			120					125				130					
acc	aaa	gtg	cag	caa	cca	ttc	aac	ctc	cct	atg	gac	agc	tgc	gtg	gcc	607	
Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala		
			135					140				145					
acc	aag	tcc	ctg	agt	ccc	gga	cac	acg	ctg	atc	ccc	agc	tca	gct	gta	655	
Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val		
					150		155			160					165		
act	ccc	cgg	gag	tca	ccc	cag	tcg	gat	tcc	ctg	ggc	tcc	acc	tac	tcc	703	
Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser		
				170					175					180			
atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa	751	
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys		
			185					190					195				
atg	gat	gac	agt	gat	cag	gat	agc	tgc	cga	cta	agc	att	gac	tca	cag	799	
Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu	Ser	Ile	Asp	Ser	Gln		
			200					205				210					
agc	agc	agc	agc	gga	ccc	cga	aag	cac	ctt	cgc	acg	gat	gcc	ttc	agc	847	
Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	Thr	Asp	Ala	Phe	Ser		
			215				220				225						
cag	cac	cac	ctc	gag	cgg	ctc	gag	tgc	cca	ttt	gag	cgg	cag	cac	tac	895	
Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr		
				230			235			240					245		
cca	gag	gcc	tat	gcc	tcc	ccc	agc	cac	acc	aaa	ggc	gag	cag	ggc	ctc	943	
Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	Gly	Glu	Gln	Gly	Leu		
				250					255					260			
tac	cgg	ctg	ccc	ttg	ctc	aac	agc	acc	ctg	gac	gac	ggg	aag	gcc	acc	991	
Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	Asp	Gly	Lys	Ala	Thr		
				265				270					275				
ctg	acc	cct	tcc	aac	acg	cca	ctg	ggg	cgc	aac	ctc	tcg	act	cac	cag	1039	
Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn	Leu	Ser	Thr	His	Gln		
			280					285				290					
acc	tac	ccc	gtg	gtg	gca	gat	cct	cac	tca	ccc	ttg	gcc	ata	aag	cag	1087	
Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro	Leu	Ala	Ile	Lys	Gln		
			295			300				305							
gaa	acc	ccc	gag	gtg	tcc	agt	tct	agc	tcc	acc	cct	tgc	tct	tta	tct	1135	

097644-0134

Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr Pro Cys Ser Leu Ser	
310 315 320 325	
agc tcc gcc ctt ttg gat ctg cag caa gtc ggc tcc ggg gtc ccg ccc	1183
Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly Ser Gly Val Pro Pro	
330 335 340	
ttc aat gcc ttt ccc cat gct gcc tcc gtg tac ggg cag ttc acg ggc	1231
Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr Gly Gln Phe Thr Gly	
345 350 355	
cag gcc ctc ctc tca ggg cga gag atg gtg ggg ccc acg ctg ccc gga	1279
Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly Pro Thr Leu Pro Gly	
360 365 370	
tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc tct	1327
Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser Ser	
375 380 385	
gcc atc gca ggc atg gtg gca gga agt gaa tac tct ggc aat gcc tat	1375
Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr Ser Gly Asn Ala Tyr	
390 395 400 405	
ggc cac acc ccc tac tcc tcc tac agc gag gcc tgg ggc ttc ccc aac	1423
Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala Trp Gly Phe Pro Asn	
410 415 420	
tcc agc ttg ctg agt tcc cca tat tat tac agt tcc aca tca agg ccg	1471
Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser Ser Thr Ser Arg Pro	
425 430 435	
agt gca ccg ccc acc act gcc acg gcc ttt gac cat ctg tagttgccat	1520
Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp His Leu	
440 445 450	
ggggacagtg ggagcgactg agcaacagga ggactcagcc tgggacaggc cccagagagt	1580
cacacaaagg aatcttttatt attacatgaa aaataaccac aagtccagca ttgcggcaca	1640
ctccctgtgt gggttaattta atgaaccatg aaagacagga tgaccttga caaggccaaa	1700
ctgtctctca agactcctta atgaggggca ggagtcccag ggaaagagaa ccatgccatg	1760
ctgaaaaaga caaaattgaa gaagaaatgt agccccagcc ggtaccctcc aaaggagaga	1820
agaagcaata gccgaggaac ttgggggggat ggcgaaatggt tccctgcccg gcccaagggt	1880
gcacagggca cctccatggc tccattatta acacaactct agcaattatg gaccataagc	1940
acttccctcc agcccacaag tcacagcctg gtgccgaggc tctgctcacc agccacccag	2000
ggagtcacct cctcagcct cccgcctgcc ccacacggag gctctggctg tctcttttc	2060
tccactccat ttgcttggt ctttctacac ctccctcttg gatgggctga gggctggagc	2120
gagtcctca gaaattccac caggctgtca gctgacctct ttttctgct gctgtgaagg	2180
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tgtggtgtgc ggcttcaccc agggcagaac aaggcagaat cgcaggaaac ccgcttcccc	2360
ttcttgacag ctcttgccaa gccaaatgtg ctctctgcag ctacgcccc ccagctactg	2420
aagggaacca aggcaccccc tgaagccagc gatagagggt cctctctgct tccccagcag	2480
ctctgcccc caaggcctga ctgtatatac tgtaaatagaa actttggttg ggtcaagctt	2540
ccttctttct aacccccaga ctttggcctc tgagtgaat gtctctctt gccctgtggg	2600
gcttctctcc ttgatgcttc tttctttttt taaagacaac ctgccattac cacatgactc	2660
aataaacctat tgctcttcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a	2711

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 <211> 450  
 <212> PRT  
 <213> Homo Sapiens

<400> 25

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Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln
			20					25					30		
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
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Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
		50				55					60				
Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys
65					70					75				80	
Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
				85					90					95	
Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
			100					105					110		
Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
		115						120					125		
Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
		130				135						140			
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
145					150					155				160	
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
				165					170					175	
Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly
		180						185					190		
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
	195					200						205			
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	
	210				215					220					
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225					230					235				240	
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
			245					250						255	
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
			260					265					270		
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
		275					280					285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro
	290				295						300				
Leu	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser	Thr
305					310					315				320	
Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
			325					330					335		
Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
			340					345					350		
Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val	Gly
		355				360						365			
Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln	Gly
	370				375						380				
Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser	Glu	Tyr
385					390					395				400	

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Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
 405 410 415  
 Trp Gly Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Ser  
 420 425 430  
 Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
 435 440 445  
 His Leu  
 450

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 <212> DNA  
 <213> Homo Sapiens  
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 <221> CDS  
 <222> (173)...(1609)

<400> 26

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 gggtctctct gagtctggga attcccagac ccgagccgca gccgccgcct ggggggcttg 120  
 ggctggcctc gaggacaccg gagaggggag ccacgccgcc gtggccgcag aa atg acc 178  
 Met Thr  
 1

atg gtt gac aca gag atc gca ttc tgg ccc acc aac ttt ggg atc agc 226  
 Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly Ile Ser  
 5 10 15

tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274  
 Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
 20 25 30

aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322  
 Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
 35 40 45 50

gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370  
 Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
 55 60 65

tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418  
 Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
 70 75 80

gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466  
 Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
 85 90 95

cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514  
 His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys  
 100 105 110

gga gat aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga 562  
 Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly  
 115 120 125 130

0975111 011801

tgc aag ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp 135 140 145	610
aga tgt gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys 150 155 160	658
cag tac tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn 165 170 175	706
gcc atc agg ttt ggg cgg atc gca cag gcc gag aag gag aag ctg ttg Ala Ile Arg Phe Gly Arg Ile Ala Gln Ala Glu Lys Glu Lys Leu Leu 180 185 190	754
gcg gag atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp 195 200 205 210	802
ctc cgt cag gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc Leu Arg Gln Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser 215 220 225	850
ttc ccg ctg acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr 230 235 240	898
aca gac aaa tca cca ttc gtt atc tat gac atg aat tcc tta atg atg Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met 245 250 255	946
gga gaa gat aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln 260 265 270	994
agc aaa gag gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser 275 280 285 290	1042
gtg gag gct gtg cag gag atc aca gag tat gcc aaa agc att cct ggt Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly 295 300 305	1090
ttt gta aat ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly 310 315 320	1138
gtc cac gag atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp 325 330 335	1186
ggg gtt ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu 340 345 350	1234

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aag agc ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag	1282
Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu	
355 360 365 370	
ttt gct gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca	1330
Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala	
375 380 385	
ata ttt att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg	1378
Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu	
390 395 400	
aat gtg aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg	1426
Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu	
405 410 415	
gag ctc cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc	1474
Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala	
420 425 430	
aag ctg ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac	1522
Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His	
435 440 445 450	
gtg cag cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt	1570
Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu	
455 460 465	
cac ccg ctc ctg cag gag atc tac aag gac ttg tac tag cagagagtcc	1619
His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr *	
470 475	
tgagccactg ccaacatttc cttcttccca gttgcactat tctgagggaa aatctgacca	1679
taagaaattt actgtgaaaa agcgtttttaa aaagaaaagg gtttagaata tgatctattt	1739
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<210> 27  
 <211> 478  
 <212> PRT  
 <213> Homo Sapiens

<400> 27
Met Thr Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly
1 5 10 15
Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe
20 25 30
Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro
35 40 45
His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp
50 55 60
Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val
65 70 75 80
Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn
85 90 95

0976544 011804



Lys	Pro	His	Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	100	105	110
Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	115	120	125
Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	130	135	140
Tyr	Asp	Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	145	150	155
Lys	Cys	Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	165	170	175
His	Asn	Ala	Ile	Arg	Phe	Gly	Arg	Ile	Ala	Gln	Ala	Glu	Lys	Glu	Lys	180	185	190
Leu	Leu	Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	195	200	205
Ala	Asp	Leu	Arg	Gln	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	210	215	220
Lys	Ser	Phe	Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	225	230	235
Lys	Thr	Thr	Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	245	250	255
Met	Met	Gly	Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	260	265	270
Glu	Gln	Ser	Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	275	280	285
Arg	Ser	Val	Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	290	295	300
Pro	Gly	Phe	Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	305	310	315
Tyr	Gly	Val	His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	325	330	335
Lys	Asp	Gly	Val	Leu	Ile	Ser	Glu	Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	340	345	350
Phe	Leu	Lys	Ser	Leu	Arg	Lys	Pro	Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	355	360	365
Phe	Glu	Phe	Ala	Val	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	370	375	380
Leu	Ala	Ile	Phe	Ile	Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	385	390	395
Leu	Leu	Asn	Val	Lys	Pro	Ile	Glu	Asp	Ile	Gln	Asp	Asn	Leu	Leu	Gln	405	410	415
Ala	Leu	Glu	Leu	Gln	Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	420	425	430
Phe	Ala	Lys	Leu	Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	435	440	445
Glu	His	Val	Gln	Leu	Leu	Gln	Val	Ile	Lys	Lys	Thr	Glu	Thr	Asp	Met	450	455	460
Ser	Leu	His	Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Lys	Asp	Leu	Tyr			465	470	475

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 <212> DNA  
 <213> Homo Sapiens

<400> 28  
 gccaccaagt ccctgagtcc

<210> 29	
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<210> 30	
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<210> 32	
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accagaaag cgattccttc a	21
<210> 33	
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atgggtgaaa ctctgggaga	20
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ttgctgcaga tccaaaaagg	20
<210> 35	
<211> 20	
<212> DNA	
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<400> 35	
gaggaagggg tggagctaga	20

0976544 011304

<210> 36  
 <211> 537  
 <212> DNA  
 <213> Homo Saiens

<220>  
 <223> n = A or T or C or G or other

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 ttc act gat aca ctg tct gca aac ata tca caa gaa nat cct cac tca 96  
 ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc 144  
 acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag caa gtc 192  
 ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg 240  
 tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag atg gtg 288  
 ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc gga cag 336  
 ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga agt gaa 384  
 tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac agc gag 432  
 gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat tat tac 480  
 agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg gcc ttt 528  
 gac cat ctg 537

<210> 37  
 <211> 348  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <223> n = A or T or C or G or other

<400> 37  
 atgggtgaaa ctctgggaga ttctcctatt gaccagaaaa gcgattcctt cactgataca 60  
 ctgtctgcaa acatatcaca agaanggcga gagatgggtg ggcccacgct gcccgataca 120  
 ccacccaca tccccaccag cggacagggc agctatgcct cctctgccat cgcaggcatg 180  
 gtggcaggaa gtgaatactc tggcaatgcc tatggccaca cccctactc ctctacagc 240  
 gaggcctggc gcttccccaa ctccagcttg ctgagttccc catattatta cagttccaca 300  
 tcaaggccga gtgcaccgcc caccactgcc acggcctttg accatctg 348

<210> 38  
 <211> 246  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <223> n = A or T or C or G or other

<400> 38  
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 ctgtctgcaa acatatcaca agaangaagt gaatactctg gcaatgccta tggccacacc 120  
 ccctactcct cctacagcga ggctggcgc tccccaaact ccagcttgct gagttcccca 180  
 tattattaca gttccacatc aaggccgagt gcaccgcca ccactgccac ggcccttgac 240  
 catctg 246

<210> 39  
 <211> 178

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<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 39

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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Xaa	Pro	His	Ser
			20					25					30		
Pro	Phe	Ala	Ile	Lys	Gln	Glu	Thr	Pro	Glu	Val	Ser	Ser	Ser	Ser	Ser
		35					40					45			
Thr	Pro	Ser	Ser	Leu	Ser	Ser	Ser	Ala	Phe	Leu	Asp	Leu	Gln	Gln	Val
	50					55					60				
Gly	Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val
65					70					75					80
Tyr	Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val
				85					90					95	
Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln
			100					105					110		
Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser	Glu
		115					120					125			
Tyr	Ser	Gly	Asn	Ala	Tyr	Gly	His	Thr	Pro	Tyr	Ser	Ser	Tyr	Ser	Glu
	130					135					140				
Ala	Trp	Arg	Phe	Pro	Asn	Ser	Ser	Leu	Leu	Ser	Ser	Pro	Tyr	Tyr	Tyr
145					150					155					160
Ser	Ser	Thr	Ser	Arg	Pro	Ala	Pro	Pro	Thr	Thr	Ala	Thr	Ala	Phe	Asp
				165					170					175	
His	Leu														

<210> 40

<211> 116

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 40

Met	Gly	Glu	Thr	Leu	Gly	Asp	Ser	Pro	Ile	Asp	Pro	Glu	Ser	Asp	Ser
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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Xaa	Arg	Glu	Met
			20					25					30		
Val	Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly
		35					40					45			
Gln	Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Gly	Ser
	50					55					60				
Glu	Tyr	Ser	Gly	Asn	Ala	Tyr	Gly	His	Thr	Pro	Tyr	Ser	Ser	Tyr	Ser
65					70					75					80
Glu	Ala	Trp	Arg	Phe	Pro	Asn	Ser	Ser	Leu	Leu	Ser	Ser	Pro	Tyr	Tyr
				85					90					95	
Tyr	Ser	Ser	Thr	Ser	Arg	Pro	Ser	Ala	Pro	Pro	Thr	Thr	Ala	Thr	Ala
			100					105					110		
Phe	Asp	His	Leu												

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<210> 41  
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<400> 41  
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1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr  
20 25 30  
Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
35 40 45  
Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser  
50 55 60  
Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
65 70 75 80  
His Leu

<210> 42  
<211> 43  
<212> DNA  
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<220>  
<223> n = A or T or C or G or other

<221> CDS  
<222> (1)...(43)

<400> 42  
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1 5 10

43

<210> 43  
<211> 14  
<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 43  
Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala  
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<210> 44  
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<213> Homo Sapiens

<220>

<223> n = A or T or C or G or other

<221> CDS

<222> (1)...(43)

<400> 44

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1 5 10

43

<210> 45

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 45

Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro  
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<210> 46

<211> 43

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<213> Homo Sapiens

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<221> CDS

<222> (1)...(43)

<400> 46

tct gca aac ata tca caa gaa nga agt gaa tac tct ggc aat g  
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43

<210> 47

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 47

Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn  
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